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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/909,775

DATE: 04/17/2002

TIME: 14:08:36

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\04172002\I909775.raw

```

4 <110> APPLICANT: Genzyme Corporation
5   Schiavi, Susan
6   Madden, Stephen L.
7   Manavalan, Parthasarathy
8   Levine, Michael
9   Jan de Beur, Suzanne
11 <120> TITLE OF INVENTION: PHOSPHATONIN-RELATED GENE AND METHODS OF
12   USE THEREOF
14 <130> FILE REFERENCE: GZ 2065.23
16 <140> CURRENT APPLICATION NUMBER: US 09/909,775
17 <141> CURRENT FILING DATE: 2001-07-19
19 <150> PRIOR APPLICATION NUMBER: US 60/219,365
20 <151> PRIOR FILING DATE: 2000-07-19
22 <150> PRIOR APPLICATION NUMBER: US 60/261,438
23 <151> PRIOR FILING DATE: 2001-01-12
25 <160> NUMBER OF SEQ ID NOS: 2
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2839
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapien
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (257)...(1297)
38 <400> SEQUENCE: 1
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40 tgccctgtgt gccagacggc ggagctccgc ggccggaccc cgcgcccccg ctttgcctgcc 120
41 gactggagtt tgggggaaga aactctcctg cgccccagaa gatttcttcc tcggcgaagg 180
42 gacagcgaaa gatgaggggtg gcaggaagag aaggcgcttt ctgtctgccg gggtcgcagc 240
43 gcgagagggc agtgcc atg ttc ctc tcc atc cta gtg gcg ctg tgc ctg tgg 292
44           Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp
45           1             5             10
47 ctg cac ctg gcg ctg ggc gtg cgc gcc gcg ccc tgc gag gcg gtg cgc 340
48 Leu His Leu Ala Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg
49           15             20             25
51 atc cct atg tgc cgg cac atg ccc tgg aac atc acg cgg atg ccc aac 388
52 Ile Pro Met Cys Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn
53           30             35             40
55 cac ctg cac cac agc acg cag gag aac gcc atc ctg gcc atc gag cag 436
56 His Leu His His Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln
57 45             50             55             60
59 tac gag gag ctg gtg gac gtg aac tgc agc gcc gtg ctg cgc ttc ttc 484
60 Tyr Glu Glu Leu Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe

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61		65		70		75		
63	ttc tgt gcc atg tac gcg ccc att tgc acc ctg gag ttc ctg cac gac							532
64	Phe Cys Ala Met Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp							
65		80		85		90		
67	cct atc aag ccg tgc aag tcg gtg tgc caa cgc gcg cgc gac gac tgc							580
68	Pro Ile Lys Pro Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys							
69		95		100		105		
71	gag ccc ctc atg aag atg tac aac cac agc tgg ccc gaa agc ctg gcc							628
72	Glu Pro Leu Met Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala							
73		110		115		120		
75	tgc gac gag ctg cct gtc tat gac cgt ggc gtg tgc att tcg cct gaa							676
76	Cys Asp Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu							
77	125		130		135		140	
79	gcc atc gtc acg gac ctc ccg gag gat gtt aag tgg ata gac atc aca							724
80	Ala Ile Val Thr Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr							
81		145		150		155		
83	cca gac atg atg gta cag gaa agg cct ctt gat gtt gac tgt aaa cgc							772
84	Pro Asp Met Met Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg							
85		160		165		170		
87	cta agc ccc gat cgg tgc aag tgt aaa aag gtg aag cca act ttg gca							820
88	Leu Ser Pro Asp Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala							
89		175		180		185		
91	acg tat ctc agc aaa aac tac agc tat gtt att cat gcc aaa ata aaa							868
92	Thr Tyr Leu Ser Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys							
93		190		195		200		
95	gct gtg cag agg agt ggc tgc aat gag gtc aca acg gtg gtg gat gta							916
96	Ala Val Gln Arg Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val							
97	205		210		215		220	
99	aaa gag atc ttc aag tcc tca tca ccc atc cct cga act caa gtc ccg							964
100	Lys Glu Ile Phe Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro							
101		225		230		235		
103	ctc att aca aat tct tct tgc cag tgt cca cac atc ctg ccc cat caa							1012
104	Leu Ile Thr Asn Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln							
105		240		245		250		
107	gat gtt ctc atc atg tgt tac gag tgg cgt tca agg atg atg ctt ctt							1060
108	Asp Val Leu Ile Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu							
109		255		260		265		
111	gaa aat tgc tta gtt gaa aaa tgg aga gat cag ctt agt aaa aga tcc							1108
112	Glu Asn Cys Leu Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser							
113		270		275		280		
115	ata cag tgg gaa gag agg ctg cag gaa cag cgg aga aca gtt cag gac							1156
116	Ile Gln Trp Glu Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp							
117	285		290		295		300	
119	aag aag aaa aca gcc ggg cgc acc agt cgt agt aat ccc ccc aaa cca							1204
120	Lys Lys Lys Thr Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro							
121		305		310		315		
123	aag gga aag cct cct gct ccc aaa cca gcc agt ccc aag aag aac att							1252
124	Lys Gly Lys Pro Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile							
125		320		325		330		

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127 aaa act agg agt gcc cag aag aga aca aac ccg aaa aga gtg tga      1297
128 Lys Thr Arg Ser Ala Gln Lys Arg Thr Asn Pro Lys Arg Val  *
129          335          340          345
131 gctaactagt ttccaaagcg gagacttccg acttcccttac aggatgaggc tgggcattgc 1357
132 ctgggacagc ctatgtaagg ccattgtgcc cttgccttaa caactcactg cagtgtctct 1417
133 catagacaca tcttgacgca tttttcttaa ggctatgctt cagtttttct ttgtaagcca 1477
134 tcacaagcca tagtggtagg ttgtcccttt ggtacagaag gtgagttaaa gctggtggaa 1537
135 aaggcttatt gcattgcatt cagagtaacc tgtgtgcata ctctagaaga gtagggaaaa 1597
136 taatgcttgt tacaattcga cctaatatgt gcattgtaaa ataaatgcca tatttcaaac 1657
137 aaaacacgta atttttttac agtatgtttt attacctttt gatatotgtt gttgcaatgt 1717
138 tagtgatgtt ttaaaatgtg atgaaaatat aatgttttta agaaggaaca gtagtggaat 1777
139 gaatgttaaa agatctttat gtgtttatgg tctgcagaag gattttttgt atgaaagggg 1837
140 attttttgaa aaattagaga agtagcatat ggaaaattat aatgtgtttt tttaccaatg 1897
141 acttcagttt ctgtttttag ctagaaactt aaaaacaaaa ataataataa agaaaaataa 1957
142 ataaaaagga gaggcagaca atgtctggat tctgtttttt tggttacctg atttccatga 2017
143 tcatgatgct tctgtcaaac accctcttaa gcagcaccag aaacagtgag tttgtctgta 2077
144 ccattaggag ttaggtacta attagttggc taatgtctca gtattttata ccacaaagag 2137
145 aggtatgtca ctcatcttac ttcccaggac atccaccctg agaataattt gacaagctta 2197
146 aaaatggcct tcatgtgagt gccaaatitt gtttttcttc atttaaatat tttctttgcc 2257
147 taaatacatg tgagaggagt taaatataaa tgtacagaga ggaaagtga gttccacctc 2317
148 tgaaatgaga attacttgac agttgggata ctttaatcag aaaaaagaa cttatttgca 2377
149 gcattttatc aacaaatttc ataattgtgg acaattggag gcattttatt taaaaacaa 2437
150 ttttattggc cttttgctaa cacagtaagc atgtatttta taaggcattc aataaatgca 2497
151 caacgcccaa aggaataaaa atcctatcta atcctactct ccactacaca gaggtaatca 2557
152 ctattagtat ttggcatat tttctccag gtgtttgctt atgcacttat aaaatgattt 2617
153 gaacaaataa aactaggaac ctgtatacat gtgtttcata acctgcctcc tttgcttggc 2677
154 cctttattga gataagtttt cctgtcaaga aagcagaaac catctcattt ctaacagctg 2737
155 tgttatatte catagtatgc attactcaac aaactgttgt gctattggat acttaggtgg 2797
156 tttcttcact gacaatactg aataaacatc tcaccggaat tc      2839
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 346
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapien
163 <400> SEQUENCE: 2
164 Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
165 1          5          10          15
166 Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
167          20          25          30
168 Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
169          35          40          45
170 Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
171          50          55          60
172 Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
173 65          70          75          80
174 Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
175          85          90          95
176 Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
177          100         105         110
178 Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu

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179	115	120	125
180	Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr		
181	130	135	140
182	Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met		
183	145	150	155
184	Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp		
185	165	170	175
186	Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser		
187	180	185	190
188	Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg		
189	195	200	205
190	Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe		
191	210	215	220
192	Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn		
193	225	230	235
194	Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile		
195	245	250	255
196	Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu		
197	260	265	270
198	Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu		
199	275	280	285
200	Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr		
201	290	295	300
202	Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro		
203	305	310	315
204	Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser		
205	325	330	335
206	Ala Gln Lys Arg Thr Asn Pro Lys Arg Val		
207	340	345	

VERIFICATION SUMMARY

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